IN THE UNITED STATES DISTRICT COURT
FOR THE MIDDLE DISTRICT OF NORTH CAROLINA

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| NATERA, INC., Plaintiff, | ) | |
| v. | ) | 1:23-CV-629 |
| NEOGENOMICS LABORATORIES INC., Defendant. | ) | |

**CLAIM CONSTRUCTION ORDER**

Natera, Inc. contends that NeoGenomics Laboratories, Inc., is infringing its patents. The parties dispute the meaning of certain terms in U.S. Patent No. 11,319,596 (the "'596 patent"), and the matter is before the Court for claim construction. The disputed claim terms are construed herein and in the attached Appendix.

## I. Introduction

Natera is the owner of the '596 patent. *See* Doc. 350-10 at 2.[1] The company uses the methods in this patent in its Signatera product, a test for early detection of cancer recurrence. Doc. 9-18 at 2–3. NeoGenomics has a competing product called RaDaR. Doc. 94 at ¶ 10; *see also* Doc. 169 at 2–4 (order giving overview of the two products).

When Natera filed the lawsuit, NeoGenomics used an assay now known in this litigation as RaDaR 1.0 and Natera alleged infringement of the '454 and '035 patents. After the Court entered a preliminary injunction prohibiting NeoGenomics from selling

[1] The Court uses the pagination appended by CM/ECF for all cites to the record.

RaDaR 1.0, NeoGenomics developed RaDaR 1.1, a method it contends does not infringe either patent. *See* Doc. 301 at 11. Infringement issues about the '035 patent and RaDaR 1.1 have been resolved, Doc. 329, and Natera now contends that RaDaR 1.1 infringes the methods claimed in the '454 patent and the '596 patent. Doc. 353 at ¶ 1. The claims in the '454 patent have long been construed. *See* Doc. 280.[2]

The parties submitted a joint claim construction statement for the '596 patent, Doc. 370, and have briefed their proposed claim constructions. Docs. 372, 373, 378, 380; see also Text Order 3/12/2025 (granting motion to supplement claim construction record). At a *Markman* hearing held on March 11, 2025, the parties presented arguments and evidence in support of their proposed constructions. Minute Entry 03/11/2025.

## II. Claim Construction

The scope of a patent is defined by its claims. *Vitronics Corp. v. Conceptronic, Inc.*, 90 F.3d 1576, 1582 (Fed. Cir. 1996). "The words of a claim are generally given their ordinary and customary meaning," which is "the meaning that the term[s] would have to a person of ordinary skill in the art in question at the time of the invention." *Phillips v. AWH Corp.*, 415 F.3d 1303, 1312–13 (Fed. Cir. 2005) (cleaned up).

A person of ordinary skill in the art views a term in the greater context of the patent itself, including the other claims and the specification. *Id.* at 1313. If it is in evidence, courts construing claims can also consider the prosecution history. *Id.* at 1317; *Vitronics*, 90 F.3d at 1582. Often the intrinsic evidence alone can reveal the meaning of a

[2] The Court denied NeoGenomics' recent motion to modify the '454 patent claim construction. Doc. 385; *see* Doc. 364.

claim term. *Vitronics*, 90 F.3d at 1583. If necessary, courts can also look to extrinsic evidence like expert testimony. *Phillips*, 415 F.3d at 1317; *see also Aristocrat Techs. Austl. Pty Ltd. v. Int'l Game Tech.*, 709 F.3d 1348, 1355, 1358 (Fed. Cir. 2013) (stating courts can consider extrinsic evidence, but there is "no reason to resort to consideration of extrinsic evidence" when claim term is clear and support is found in specification).

## III. Disputed Claim Terms

The parties dispute the meaning of several terms in claim 1 of the '596 patent. With the disputed terms highlighted in yellow, claim 1 states:

> A method for preparing biological samples useful for monitoring the progression of cancer in a subject, the method comprising:
> (a) performing sequencing on a tumor biopsy sample of the subject to identify a plurality of tumor-specific mutations, wherein the tumor-specific mutations comprise one or more single nucleotide variant (SNV) mutations;
> (b) evaluating results of the sequencing on the tumor biopsy sample to determine a plurality of target loci specific to the subject, wherein each target locus spans a tumor-specific mutation of the identified plurality of tumor-specific mutations; and
> (c) assaying cell-free DNA isolated from a plurality of biological samples obtained from the subject at different time points, wherein the assaying comprises:
> performing targeted multiplex PCR amplification to amplify the plurality of target loci together in the same reaction volume from the isolated cell-free DNA using primers specific to the plurality of target loci for the individual subject; and
> performing high-throughput sequencing of the amplified DNA comprising the plurality of target loci to obtain sequence reads, wherein an SNV mutation that is present in less than or equal to 0.015% of the cell-free DNA having the SNV locus is detected from the sequence reads.

Doc. 350-10 at 220.

### A. "the isolated cell-free DNA"

The parties dispute the meaning of the terms "the isolated cell-free DNA." Their proposed constructions are below:

| Claim | Natera's Construction | NeoGenomics' Construction |
|---|---|---|
| "the isolated cell-free DNA" | Plain and ordinary meaning, which includes cell-free DNA isolated from any of the plurality of biological samples obtained from the subject at different time points | Plain and ordinary meaning, which is cell-free DNA isolated from a plurality of biological samples obtained from the subject |

Doc. 370-1 at 1.

Natera contends that its construction, by including the word "any," properly allows "the isolated cell-free DNA" that is being amplified to include DNA "isolated from a single biological sample." Doc 372 at 9–10. NeoGenomics contends that the language of claim 1 requires "the isolated cell-free DNA" to come from "multiple samples." Doc. 373 at 16.

The Court agrees with Natera. NeoGenomics' construction would "read unstated limitations into claim language." *See N. Telecom Ltd. v. Samsung Elecs. Co.*, 215 F.3d 1281, 1290 (Fed. Cir. 2000). Further, claim 17 of the patent depends on claim 1 and contemplates a single sample: "The method of claim 1, wherein the biological sample is a blood, serum, plasma, or urine sample." Doc. 350-10 at 220. "[I]f a dependent claim reads on a particular embodiment of the claimed invention, the corresponding independent claim must cover that embodiment as well." *Littelfuse, Inc. v. Mersen USA*

*EP Corp.*, 29 F.4th 1376, 1380 (Fed. Cir. 2022). Thus claim 1 must allow amplification of DNA from a single sample.

The Court adopts Natera's construction.

**B. "performing high-throughput sequencing of the amplified DNA"**

The parties dispute the meaning of the terms "performing high-throughput sequencing of the amplified DNA." Their proposed constructions are below:

| Claim | Natera's Construction | NeoGenomics' Construction |
|---|---|---|
| "performing high-throughput sequencing of the amplified DNA" | Plain and ordinary meaning, which permits intermediate steps after multiplex amplification but before sequencing | Plain and ordinary meaning, which is performing high-throughput sequencing of the amplified DNA obtained from the targeted multiplex PCR amplification step |

Doc. 370-1 at 9.

Natera contends that the Court should construe these terms consistently with its previous construction of similar terms in the '454 patent. Doc. 372 at 21–22; *see also* Doc. 280 at 7–10. NeoGenomics makes the same arguments that it made in support of its recent motion to modify the '454 patent claim construction for those similar terms. Doc. 373 at 25–27; *see also* Doc. 365 at 5–6. The Court denied that motion, Doc. 385, and for the same reasons, the Court here adopts Natera's construction.

**C. "performing high-throughput sequencing . . . , wherein an SNV mutation . . . is detected from the sequence reads" and "wherein an SNV mutation . . . is detected from the sequence reads"**

The parties dispute the meaning of the terms "performing high-throughput sequencing of the amplified DNA comprising the plurality of target loci to obtain

sequence reads, wherein an SNV mutation that is present in less than or equal to 0.015% of the cell-free DNA having the SNV locus is detected from the sequence reads." They also dispute the meaning of the last half of these terms, the clause "wherein an SNV mutation . . . is detected from the sequence reads." Their proposed constructions are below:

| Claim | Natera's Construction | NeoGenomics' Construction |
|---|---|---|
| "performing high-throughput sequencing of the amplified DNA comprising the plurality of target loci to obtain sequence reads, wherein an SNV mutation that is present in less than or equal to 0.015% of the cell-free DNA having the SNV locus is detected from the sequence reads" | Plain and ordinary meaning, which means that the terms are part of the "performing high-throughput sequencing . . . to obtain sequence reads" step and the "wherein" clause informs the mechanics of how the high-throughput sequencing is performed | Plain and ordinary meaning, no construction necessary beyond the constructions of Terms 3 and 4 below[3] |
| "wherein an SNV mutation . . . is detected from the sequence reads" | (same as above) | Plain and ordinary meaning, which is wherein an SNV mutation is determined to be present from the sequence reads |

Doc. 370-1 at 7–8, 11.

Natera contends that "[t]he claim's punctuation, grammar, and syntax" support its proposed construction of these terms as describing one step. Doc. 372 at 17. NeoGenomics contends that the parties' only disputes about these terms relate to the

[3] Term 3 refers to "performing high-throughput sequencing of the amplified DNA," Doc. 370-1 at 9, which the Court construed *supra*, and Term 4 refers to "wherein an SNV mutation . . . is detected from the sequence reads." *Id.* at 11.

meaning of certain portions of them, Doc. 373 at 17–18, and that construction of additional words surrounding those portions would not be helpful to the jury. Doc. 380 at 11–12. And as to the "wherein" clause, NeoGenomics contends that the plain language of the claim requires that "the information in the sequence reads is obtained first, and that information is used to detect an SNV mutation." Doc. 373 at 18–19, 23–24.

The Court agrees with Natera. "A claim must be read in accordance with the precepts of English grammar." *In re Hyatt*, 708 F.2d 712, 714 (Fed. Cir. 1983); *see also Mformation Techs., Inc. v. Rsch. in Motion Ltd.*, 764 F.3d 1392, 1398 (Fed. Cir. 2014) (holding a claim may, "as a matter of logic or grammar," require an order of steps); *Tris Pharma, Inc. v. Teva Pharms. USA, Inc.*, No. 20-CV-5212, 2021 WL 3879153, at *3 (D.N.J. Aug. 25, 2021) (stating a person of ordinary skill in the art "still follows the basics of English"). A claim does not require an order of steps unless it recites an order, the specification requires an order, or an order is clearly required by the rules of grammar or logic. *Mformation*, 764 F.3d at 1398.

The grammar and structure of claim 1 suggest that these terms should be read as a whole to describe one step. Claim 1 contains three general steps, denoted as (a), (b), and (c), which are separated by semicolons. Doc. 350-10 at 220. The terms "performing high-throughput sequencing . . . , wherein an SNV mutation . . . is detected from the sequence reads" comprise the second step of step (c), as shown by the fact that the two discrete portions under step (c), which each begin with the word "performing," have hanging indents and are separated by a semicolon. *Id.* The clause "wherein an SNV mutation . . . is detected from the sequence reads" is included in the second step of step

(c) and is only offset by a comma. *Id.* Thus, detection of an SNV mutation is part of the sequencing step.[4]

NeoGenomics contends that detection requires more, including data processing to get rid of "noise." Doc. 373 at 20. But the claim does not mention noise or data processing, and the Court will not "read unstated limitations into claim language." *See N. Telecom Ltd.*, 215 F.3d at 1290.

While the Court agrees with Natera, it found Natera's proposed wording clunky and confusing. The Court construes the term to have its "plain and ordinary meaning, which means this term is read as a whole and describes one sequencing step." And the Court construes the term "wherein an SNV mutation . . . is detected from the sequence reads" to have its "plain and ordinary meaning, which includes that detection is part of sequencing."

It is **ORDERED** that the claims at issue are **CONSTRUED** as set forth herein and as summarized in the attached chart.

This the 17th day of March, 2025.

UNITED STATES DISTRICT JUDGE

[4] This dispute is similar to the parties' dispute over the '454 patent terms "sequencing the amplicons to obtain sequence reads, and detecting one or more of the tumor-specific SNV mutations present in the cell-free DNA from the sequence reads." *See* Doc. 280 at 10. The Court construed those terms to mean that "the sequencing and detecting are all part of one sequencing step" because of the grammar and structure of the claim. *Id.* at 10–11. The terms here have the same structure that led to the Court's construction of the similar '454 patent terms. *Compare* Doc. 350-10 at 220, *with* Doc. 1-1 at 222.

**Appendix**

| Claim | Natera's Proposed Construction | NeoGenomics' Proposed Construction | Court's Construction |
|---|---|---|---|
| "the isolated cell-free DNA" | Plain and ordinary meaning, which includes cell-free DNA isolated from any of the plurality of biological samples obtained from the subject at different time points | Plain and ordinary meaning, which is cell-free DNA isolated from a plurality of biological samples obtained from the subject | Plain and ordinary meaning, which includes cell-free DNA isolated from any of the plurality of biological samples obtained from the subject at different time points |
| "performing high-throughput sequencing of the amplified DNA comprising the plurality of target loci to obtain sequence reads, wherein an SNV mutation that is present in less than or equal to 0.015% of the cell-free DNA having the SNV locus is detected from the sequence reads" | Plain and ordinary meaning, which means that the terms are part of the "performing high-throughput sequencing . . . to obtain sequence reads" step and the "wherein" clause informs the mechanics of how the high-throughput sequencing is performed | Plain and ordinary meaning, no construction necessary beyond the constructions of Terms 3 and 4 below | Plain and ordinary meaning, which means this term is read as a whole and describes one sequencing step |

| Claim | Natera's Proposed Construction | NeoGenomics' Proposed Construction | Court's Construction |
|---|---|---|---|
| "performing high-throughput sequencing of the amplified DNA" | Plain and ordinary meaning, which permits intermediate steps after multiplex amplification but before sequencing | Plain and ordinary meaning, which is performing high-throughput sequencing of the amplified DNA obtained from the targeted multiplex PCR amplification step | Plain and ordinary meaning, which permits intermediate steps after multiplex amplification but before sequencing |
| "wherein an SNV mutation . . . is detected from the sequence reads" | Plain and ordinary meaning, which means that the terms are part of the "performing high-throughput sequencing . . . to obtain sequence reads" step and the "wherein" clause informs the mechanics of how the high-throughput sequencing is performed | Plain and ordinary meaning, which is wherein an SNV mutation is determined to be present from the sequence reads | Plain and ordinary meaning, which includes that detection is part of sequencing |